

## SEQUENCE LISTING

<110> UAB Research Foundation  
van Ginkel, Frederik W.  
Briles, David E.  
Watt, James M.

<120> COMPOSITION FOR REDUCING BACTERIAL  
CARRIAGE AND CNS INVASION AND METHODS OF USING SAME

<130> 21085.0067P1

<150> 60/518,799

<151> 2003-11-10

<160> 17

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
Synthetic Construct

<400> 1

atttctgtaa cagctaccaa cga

23

<210> 2

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
Synthetic Construct

<400> 2

gaattccctg tcttttcaaa gtc

23

<210> 3

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
Synthetic Construct

<400> 3

ccgatacaact ctcttcccga

20

<210> 4

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
Synthetic Construct

<400> 4

acagttgggtg ctaaggagggc

20

<210> 5

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
Synthetic Construct

<400> 5

Val	Trp	Arg	Leu	Leu	Ala	Pro	Pro	Phe	Ser	Asn	Arg	Leu	Leu	Pro
1				5				10					15	

<210> 6

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
Synthetic Construct

<400> 6

cgcggatcct catactgggt taggaaagtc gtcg

34

<210> 7

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
Synthetic Construct

<400> 7

ggaattccat atgccgacag cagaactacc taaaggc

37

<210> 8

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
Synthetic Construct

<400> 8

ggaattccat atgctggcaa atgaaactca actttcgggg g

41

<210> 9

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
Synthetic Construct

<400> 9

cgcggatcca tcggctttga ccatcggag

29

<210> 10

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
Synthetic Construct

<400> 10

ggaattccat atgcgtattc cagcacttct caagacag

38

<210> 11

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
Synthetic Construct

<400> 11

ggaacattac ctcgcaaaag g

21

<210> 12

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
Synthetic Construct

<400> 12

tacccgcagg cataacatc

19

<210> 13

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
Synthetic Construct

<400> 13

Leu Pro Glu Thr Gly

1

5

<210> 14

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
Synthetic Construct

<221> VARIANT

<222> 3

<223> Xaa = any amino acid.

<400> 14

Leu Pro Xaa Thr Gly  
1 5

<210> 15

<211> 1035

<212> PRT

<213> S. pneumoniae

<400> 15

Met	Ser	Tyr	Phe	Arg	Asn	Arg	Asp	Ile	Asp	Ile	Glu	Arg	Asn	Ser	Met
1				5					10					15	
Asn	Arg	Ser	Val	Gln	Glu	Arg	Lys	Cys	Arg	Tyr	Ser	Ile	Arg	Lys	Leu
			20					25					30		
Ser	Val	Gly	Ala	Val	Ser	Met	Ile	Val	Gly	Ala	Val	Val	Phe	Gly	Thr
		35					40					45			
Ser	Pro	Val	Leu	Ala	Gln	Glu	Gly	Ala	Ser	Glu	Gln	Pro	Leu	Ala	Asn
	50					55					60				
Glu	Thr	Gln	Leu	Ser	Gly	Glu	Ser	Ser	Thr	Leu	Thr	Asp	Thr	Glu	Lys
65					70					75				80	
Ser	Gln	Pro	Ser	Ser	Glu	Thr	Glu	Leu	Ser	Gly	Asn	Lys	Gln	Glu	Gln
				85					90					95	
Glu	Arg	Lys	Asp	Lys	Gln	Glu	Glu	Lys	Ile	Pro	Arg	Asp	Tyr	Tyr	Ala
			100					105					110		
Arg	Asp	Leu	Glu	Asn	Val	Glu	Thr	Val	Ile	Glu	Lys	Glu	Asp	Val	Glu
			115					120					125		
Thr	Asn	Ala	Ser	Asn	Gly	Gln	Arg	Val	Asp	Leu	Ser	Ser	Glu	Leu	Asp
			130			135						140			
Lys	Leu	Lys	Lys	Leu	Glu	Asn	Ala	Thr	Val	His	Met	Glu	Phe	Lys	Pro
145					150					155				160	
Asp	Ala	Lys	Ala	Pro	Ala	Phe	Tyr	Asn	Leu	Phe	Ser	Val	Ser	Ser	Ala
				165					170					175	
Thr	Lys	Lys	Asp	Glu	Tyr	Phe	Thr	Met	Ala	Val	Tyr	Asn	Asn	Thr	Ala
			180					185					190		
Thr	Leu	Glu	Gly	Arg	Gly	Ser	Asp	Gly	Lys	Gln	Phe	Tyr	Asn	Asn	Tyr
		195					200					205			
Asn	Asp	Ala	Pro	Leu	Lys	Val	Lys	Pro	Gly	Gln	Trp	Asn	Ser	Val	Thr
		210				215						220			
Phe	Thr	Val	Glu	Lys	Pro	Thr	Ala	Glu	Leu	Pro	Lys	Gly	Arg	Val	Arg
225					230					235				240	
Leu	Tyr	Val	Asn	Gly	Val	Leu	Ser	Arg	Thr	Ser	Leu	Arg	Ser	Gly	Asn
				245					250					255	
Phe	Ile	Lys	Asp	Met	Pro	Asp	Val	Thr	His	Val	Gln	Ile	Gly	Ala	Thr
			260					265					270		
Lys	Arg	Ala	Asn	Asn	Thr	Val	Trp	Gly	Ser	Asn	Leu	Gln	Ile	Arg	Asn
		275					280					285			
Leu	Thr	Val	Tyr	Asn	Arg	Ala	Leu	Thr	Pro	Glu	Glu	Val	Gln	Lys	Arg
		290				295						300			
Ser	Gln	Leu	Phe	Lys	Arg	Ser	Asp	Leu	Glu	Lys	Lys	Leu	Pro	Glu	Gly
305					310					315					320

Ala Ala Leu Thr Glu Lys Thr Asp Ile Phe Glu Ser Gly Arg Asn Gly  
 325 330 335  
 Lys Pro Asn Lys Asp Gly Ile Lys Ser Tyr Arg Ile Pro Ala Leu Leu  
 340 345 350  
 Lys Thr Asp Lys Gly Thr Leu Ile Ala Gly Ala Asp Glu Arg Arg Leu  
 355 360 365  
 His Ser Ser Asp Trp Gly Asp Ile Gly Met Val Ile Arg Arg Ser Glu  
 370 375 380  
 Asp Asn Gly Lys Thr Trp Gly Asp Arg Val Thr Ile Thr Asn Leu Arg  
 385 390 395 400  
 Asp Asn Pro Lys Ala Ser Asp Pro Ser Ile Gly Ser Pro Val Asn Ile  
 405 410 415  
 Asp Met Val Leu Val Gln Asp Pro Glu Thr Lys Arg Ile Phe Ser Ile  
 420 425 430  
 Tyr Asp Met Phe Pro Glu Gly Lys Gly Ile Phe Gly Met Ser Ser Gln  
 435 440 445  
 Lys Glu Glu Ala Tyr Lys Lys Ile Asp Gly Lys Thr Tyr Gln Ile Leu  
 450 455 460  
 Tyr Arg Glu Gly Glu Lys Gly Ala Tyr Thr Ile Arg Glu Asn Gly Thr  
 465 470 475 480  
 Val Tyr Thr Pro Asp Gly Lys Ala Thr Asp Tyr Arg Val Val Val Asp  
 485 490 495  
 Pro Val Lys Pro Ala Tyr Ser Asp Lys Gly Asp Leu Tyr Lys Gly Asn  
 500 505 510  
 Gln Leu Leu Gly Asn Ile Tyr Phe Thr Thr Asn Lys Thr Ser Pro Phe  
 515 520 525  
 Arg Ile Ala Lys Asp Ser Tyr Leu Trp Met Ser Tyr Ser Asp Asp Asp  
 530 535 540  
 Gly Lys Thr Trp Ser Ala Pro Gln Asp Ile Thr Pro Met Val Lys Ala  
 545 550 555 560  
 Asp Trp Met Lys Phe Leu Gly Val Gly Pro Gly Thr Gly Ile Val Leu  
 565 570 575  
 Arg Asn Gly Pro His Lys Gly Arg Ile Leu Ile Pro Val Tyr Thr Thr  
 580 585 590  
 Asn Asn Val Ser His Leu Asn Gly Ser Gln Ser Ser Arg Ile Ile Tyr  
 595 600 605  
 Ser Asp Asp His Gly Lys Thr Trp His Ala Gly Glu Ala Val Asn Asp  
 610 615 620  
 Asn Arg Gln Val Asp Gly Gln Lys Ile His Ser Ser Thr Met Asn Asn  
 625 630 635 640  
 Arg Arg Ala Gln Asn Thr Glu Ser Thr Val Val Gln Leu Asn Asn Gly  
 645 650 655  
 Asp Val Lys Leu Phe Met Arg Gly Leu Thr Gly Asp Leu Gln Val Ala  
 660 665 670  
 Thr Ser Lys Asp Gly Gly Val Thr Trp Glu Lys Asp Ile Lys Arg Tyr  
 675 680 685  
 Pro Gln Val Lys Asp Val Tyr Val Gln Met Ser Ala Ile His Thr Met  
 690 695 700  
 His Glu Gly Lys Glu Tyr Ile Ile Leu Ser Asn Ala Gly Gly Pro Lys  
 705 710 715 720  
 Arg Glu Asn Gly Met Val His Leu Ala Arg Val Glu Glu Asn Gly Glu  
 725 730 735  
 Leu Thr Trp Leu Lys His Asn Pro Ile Gln Lys Gly Glu Phe Ala Tyr  
 740 745 750  
 Asn Ser Leu Gln Glu Leu Gly Asn Gly Glu Tyr Gly Ile Leu Tyr Glu  
 755 760 765  
 His Thr Glu Lys Gly Gln Asn Ala Tyr Thr Leu Ser Phe Arg Lys Phe  
 770 775 780  
 Asn Trp Asp Phe Leu Ser Lys Asp Leu Ile Ser Pro Thr Glu Ala Lys  
 785 790 795 800

Val Lys Arg Thr Arg Glu Met Gly Lys Gly Val Ile Gly Leu Glu Phe  
 805 810 815  
 Asp Ser Glu Val Leu Val Asn Lys Ala Pro Thr Leu Gln Leu Ala Asn  
 820 825 830  
 Gly Lys Thr Ala Arg Phe Met Thr Gln Tyr Asp Thr Lys Thr Leu Leu  
 835 840 845  
 Phe Thr Val Asp Ser Glu Asp Met Gly Gln Lys Val Thr Gly Leu Ala  
 850 855 860  
 Glu Gly Ala Ile Glu Ser Met His Asn Leu Pro Val Ser Val Ala Gly  
 865 870 875 890  
 Thr Lys Leu Ser Asn Gly Met Asn Gly Ser Glu Ala Ala Val His Glu  
 885 895  
 Val Pro Glu Tyr Thr Gly Pro Leu Gly Thr Ser Gly Glu Glu Pro Ala  
 900 905 910  
 Pro Thr Val Glu Lys Pro Glu Tyr Thr Gly Pro Leu Gly Thr Ser Gly  
 915 920 925  
 Glu Glu Pro Ala Pro Thr Val Glu Lys Pro Glu Tyr Thr Gly Pro Leu  
 930 935 940  
 Gly Thr Ala Gly Glu Glu Ala Ala Pro Thr Val Glu Lys Pro Glu Phe  
 945 950 955 960  
 Thr Gly Gly Val Asn Gly Thr Glu Pro Ala Val His Glu Ile Ala Glu  
 965 970 975  
 Tyr Lys Gly Ser Asp Ser Leu Val Thr Leu Thr Thr Lys Glu Asp Tyr  
 980 985 990  
 Thr Tyr Lys Ala Pro Leu Ala Gln Gln Ala Leu Pro Glu Thr Gly Asn  
 995 1000 1005  
 Lys Glu Ser Asp Leu Leu Ala Ser Leu Gly Leu Thr Ala Phe Phe Leu  
 1010 1015 1020  
 Gly Leu Phe Thr Leu Gly Lys Lys Arg Glu Gln  
 1025 1030 1035

<210> 16  
 <211> 962  
 <212> PRT  
 <213> S. pneumoniae

<400> 16  
 Met Asn Arg Ser Val Gln Glu Arg Lys Cys Arg Tyr Ser Ile Arg Lys  
 1 5 10 15  
 Leu Ser Val Gly Ala Val Ser Met Ile Val Gly Ala Val Val Asn Gly  
 20 25 30  
 Thr Ser Pro Val Leu Ala Gln Glu Gly Ala Ser Glu Gln Pro Leu Ala  
 35 40 45  
 Asn Glu Thr Gln Leu Ser Gly Glu Ser Ser Thr Leu Thr Asp Thr Glu  
 50 55 60  
 Lys Ser Gln Pro Ser Ser Glu Thr Glu Leu Ser Gly Asn Lys Gln Glu  
 65 70 75 80  
 Gln Glu Arg Lys Asp Lys Gln Glu Glu Lys Ile Pro Arg Asp Tyr Tyr  
 85 90 95  
 Ala Arg Asp Leu Glu Asn Val Glu Thr Val Ile Glu Lys Glu Asp Val  
 100 105 110  
 Glu Thr Asn Ala Ser Asn Gly Gln Arg Val Asp Leu Ser Ser Glu Leu  
 115 120 125  
 Asp Lys Leu Lys Lys Leu Glu Asn Ala Thr Val His Met Glu Asn Lys  
 130 135 140  
 Pro Asp Ala Lys Ala Pro Ala Phe Tyr Asn Leu Asn Ser Val Ser Ser  
 145 150 155 160  
 Ala Thr Lys Lys Asp Glu Tyr Phe Thr Met Ala Val Tyr Asn Asn Thr  
 165 170 175

Ala Thr Leu Glu Gly Arg Gly Ser Asp Gly Lys Gln Asn Tyr Asn Asn  
 180 185 190  
 Tyr Asn Asp Ala Pro Leu Lys Val Lys Pro Gly Gln Trp Asn Ser Val  
 195 200 205  
 Thr Phe Thr Val Glu Lys Pro Thr Ala Glu Leu Pro Lys Gly Arg Val  
 210 215 220  
 Arg Leu Tyr Val Asn Gly Val Leu Ser Arg Thr Ser Leu Arg Ser Gly  
 225 230 235 240  
 Asn Phe Ile Lys Asp Met Pro Asp Val Thr His Val Gln Ile Gly Ala  
 245 250 255  
 Thr Lys Arg Ala Asn Asn Thr Val Trp Gly Ser Asn Leu Gln Ile Arg  
 260 265 270  
 Asn Leu Thr Val Tyr Asn Arg Ala Leu Thr Pro Glu Glu Val Gln Lys  
 275 280 285  
 Arg Ser Gln Leu Asn Lys Arg Ser Asp Leu Glu Lys Lys Leu Pro Glu  
 290 295 300  
 Gly Ala Ala Leu Thr Glu Lys Thr Asp Ile Phe Glu Ser Gly Arg Asn  
 305 310 315 320  
 Gly Asn Pro Asn Lys Asp Gly Ile Lys Ser Tyr Arg Ile Pro Ala Leu  
 325 330 335  
 Leu Lys Thr Asp Lys Gly Thr Leu Ile Ala Gly Ala Asp Glu Arg Arg  
 340 345 350  
 Leu His Ser Ser Asp Trp Gly Asp Ile Gly Met Val Ile Arg Arg Ser  
 355 360 365  
 Glu Asp Asn Gly Lys Thr Trp Gly Asp Arg Val Thr Ile Thr Asn Leu  
 370 375 380  
 Arg Asp Asn Pro Lys Ala Ser Asp Pro Ser Ile Gly Ser Pro Val Asn  
 385 390 395 400  
 Ile Asp Met Val Leu Val Gln Asp Pro Glu Thr Lys Arg Ile Asn Ser  
 405 410 415  
 Ile Tyr Asp Met Phe Pro Glu Gly Lys Gly Ile Asn Gly Met Ser Ser  
 420 425 430  
 Gln Lys Glu Glu Ala Tyr Lys Lys Ile Asp Gly Lys Thr Tyr Gln Ile  
 435 440 445  
 Leu Tyr Arg Glu Gly Glu Lys Gly Ala Tyr Thr Ile Arg Glu Asn Gly  
 450 455 460  
 Thr Val Tyr Thr Pro Asp Gly Lys Ala Thr Asp Tyr Arg Val Val Val  
 465 470 475 480  
 Asp Pro Val Lys Pro Ala Tyr Ser Asp Lys Gly Asp Leu Tyr Lys Gly  
 485 490 495  
 Asp Gln Leu Leu Gly Asn Ile Tyr Phe Thr Thr Asn Lys Thr Ser Pro  
 500 505 510  
 Asn Arg Ile Ala Lys Asp Ser Tyr Leu Trp Met Ser Tyr Ser Asp Asp  
 515 520 525  
 Asp Gly Lys Thr Trp Ser Ala Pro Gln Asp Ile Thr Pro Met Val Lys  
 530 535 540  
 Ala Asp Trp Met Lys Phe Leu Gly Val Gly Pro Gly Thr Gly Ile Val  
 545 550 555 560  
 Leu Arg Asn Gly Pro His Lys Gly Arg Ile Leu Ile Pro Val Tyr Thr  
 565 570 575  
 Thr Asn Asn Val Ser His Leu Asp Gly Ser Gln Ser Ser Arg Val Ile  
 580 585 590  
 Tyr Ser Asp Asp His Gly Lys Thr Trp His Ala Gly Glu Ala Val Asn  
 595 600 605  
 Asp Asn Arg Gln Val Asp Gly Gln Lys Ile His Ser Ser Thr Met Asn  
 610 615 620  
 Asn Arg Arg Ala Gln Asn Thr Glu Ser Thr Val Val Gln Leu Asn Asn  
 625 630 635 640  
 Gly Asp Val Lys Leu Asn Met Arg Gly Leu Thr Gly Asp Leu Gln Val  
 645 650 655

Ala Thr Ser Lys Asp Gly Gly Val Thr Trp Glu Lys Asp Ile Lys Arg  
 660 665 670  
 Tyr Pro Gln Val Lys Asp Val Tyr Val Gln Met Ser Ala Ile His Thr  
 675 680 685  
 Met His Glu Gly Lys Glu Tyr Ile Ile Leu Ser Asn Ala Gly Gly Pro  
 690 695 700  
 Lys Arg Glu Asn Gly Met Val His Leu Ala Arg Val Glu Glu Asn Gly  
 705 710 715 720  
 Glu Leu Thr Trp Leu Lys His Asn Pro Ile Gln Lys Gly Glu Asn Ala  
 725 730 735  
 Tyr Asn Ser Leu Gln Glu Leu Gly Asn Gly Glu Tyr Gly Ile Leu Tyr  
 740 745 750  
 Glu His Thr Glu Lys Gly Gln Asn Ala Tyr Thr Leu Ser Asn Arg Lys  
 755 760 765  
 Asn Asn Trp Glu Asn Leu Ser Lys Asn Leu Ile Ser Pro Thr Glu Ala  
 770 775 780  
 Asn Asn Arg Asp Gly Gln Arg Arg Asp Gly Gln Arg Ser Tyr Trp Leu  
 785 790 795 800  
 Gly Val Arg Leu Arg Ser Ile Gly Gln Gln Gly Ser Asn Pro Ser Ile  
 805 810 815  
 Gly Lys Trp Asn Asn Ser Asp Asn Pro Asn Pro Val Asn Asn Gln Asp  
 820 825 830  
 Leu Val Val Cys Ser Arg Asn Gly Arg Tyr Arg Thr Gly Asn Tyr Trp  
 835 840 845  
 Tyr Ser Asn Arg Lys His Arg Lys Tyr Ala Asn Ser Ser Cys Lys Ser  
 850 855 860  
 Ser Arg Cys Gln Ser Ser Trp Arg Ser Lys Trp Asn Gln Ser Ser Gly  
 865 870 875 880  
 Ala Asn Ser Ser Arg Ile Tyr Arg Gly Ser Asn Trp Tyr Arg Ala Ser  
 885 890 895  
 Cys Ser Asn Asn Arg Arg Val Asn Gly Ile Asn Phe Ala Cys Asn Ser  
 900 905 910  
 Tyr Tyr Lys Lys Arg Leu Tyr Leu Gln Ser Ser Ser Cys Ser Ala Gly  
 915 920 925  
 Thr Ser Asn Asn Arg Lys Gln Gly Glu Asn Pro Pro Ser Phe Thr Arg  
 930 935 940  
 Thr Asn Ser Asn Leu Pro Trp Ser Val Tyr Ala Arg Glu Lys Glu Arg  
 945 950 955 960  
 Thr Ile

&lt;210&gt; 17

&lt;211&gt; 382

&lt;212&gt; PRT

<213> *S. typhimurium*

&lt;400&gt; 17

Met Thr Val Glu Lys Ser Val Val Phe Lys Ala Glu Gly Glu His Phe  
 1 5 10 15  
 Thr Asp Gln Lys Gly Asn Thr Ile Val Gly Ser Gly Ser Gly Thr  
 20 25 30  
 Thr Lys Tyr Phe Arg Ile Pro Ala Met Cys Thr Thr Ser Lys Gly Thr  
 35 40 45  
 Ile Val Val Phe Ala Asp Ala Arg His Asn Thr Ala Ser Asp Gln Ser  
 50 55 60  
 Phe Ile Asp Thr Ala Ala Arg Ser Thr Asp Gly Gly Lys Thr Trp  
 65 70 75 80  
 Asn Lys Lys Ile Ala Ile Tyr Asn Asp Arg Val Asn Ser Lys Leu Ser  
 85 90 95  
 Arg Val Met Asp Pro Thr Cys Ile Val Ala Asn Ile Gln Gly Arg Glu  
 100 105 110  
 Thr Ile Leu Val Met Val Gly Lys Trp Asn Asn Asn Asp Lys Thr Trp



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